

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
5 April 2001 (05.04.2001)

PCT

(10) International Publication Number
WO 01/23582 A1(51) International Patent Classification⁷: C12N 15/55,
15/61, C12P 13/00, 13/22, 41/00, C12N 1/21, C12Q 1/68

(21) International Application Number: PCT/EP00/08473

(22) International Filing Date: 31 August 2000 (31.08.2000)

(25) Filing Language: English

(26) Publication Language: English

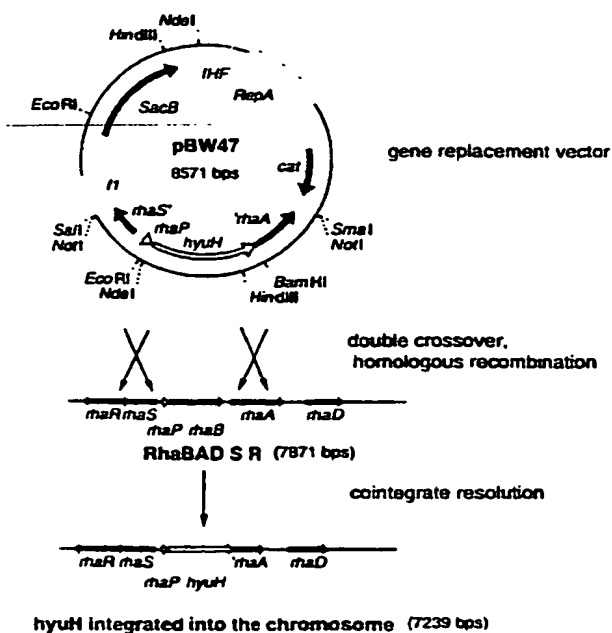
(30) Priority Data:
09/407,062 28 September 1999 (28.09.1999) US(71) Applicants: DEGUSSA-HÜLS AKTIENGE-
SELLSCHAFT [DE/DE]; 60287 Frankfurt am Main
(DE). UNIVERSITÄT STUTTGART [DE/DE]; Al-
lmandring 31, 70569 Stuttgart (DE). ROCHE DIAGNOS-
TICS GMBH [DE/DE]; Sandhofer Strasse 116, 68298
Mannheim (DE).(72) Inventors: ALTENBUCHNER, Josef; Hinden-
burgstrasse 6, 71154 Nufringen (DE). MATTES, Ralf;
Friedrich-Zundel-Strasse 14, 70619 Stuttgart (DE).
SYLDATK, Christoph; Reinbeckstrasse 29B, 70565Stuttgart (DE). WIESE, Anja; Hauptstrasse 11a, 85386
Eching (DE). WILMS, Burkard; Robert-Leicht-Strasse
37b, 70563 Stuttgart (DE). BOMMARIUS, Andreas;
Waidmannstrasse 7-9, 60596 Frankfurt am Main (DE).
TISCHER, Wilhelm; Finkenweg 5, 82380 Peissenberg
(DE).(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG-SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— With international search report.
— With amended claims.

[Continued on next page]

(54) Title: WHOLE CELL CATALYST COMPRISING A HYDANTOINASE, A RACEMASE AND A CARBAMOYLASE

Chromosomal insertion of *hyuH*(57) Abstract: A whole cell catalyst is described comprising a
hydantoinase, a racemase and a carbamoylase. Thus this cata-
lyst is able to degrade hydantoins directly into the amino acids.
Additionally, a process for the production of these catalysts and
for the production of amino acids is claimed.

WO 01/23582 A1



— *With (an) indication(s) in relation to deposited biological material furnished under Rule 13bis separately from the description.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WHOLE CELL CATALYST COMPRISING A HYDANTOINASE, A RACEMASE AND A CARBAMOYLASE

The present invention is directed to a micro-organism, which is able to degrade hydantoins to enantiomerically enriched amino acids. Especially, this micro-organism is
5 equipped with cloned genes coding for the necessary enzymes.

Racemic 5-monosubstituted hydantoins can be chemically synthesized according to Bucherer-Berg method using aldehydes, ammonium bicarbonate and sodium cyanide as
10 reactants. They are important precursors for the enzymatic production of D-and L- amino acids. With the increasing demand for optically pure amino acids a lot of effort has been made towards the isolation of microorganisms capable for stereospecific hydrolysis of the hydantoins and
15 characterization of the enzymes (Syldatk and Pietzsch, "Hydrolysis and formation of hydantoins" (1995), VCH Verlag, Weinheim, pp. 403-434; Ogawa et al., J. Mol. Catal. B: Enzym 2 (1997), 163-176; Syldatk et al., Appl. Microbiol. Biotechnol. 51 (1999), 293-309). The asymmetric
20 bio-conversion to either L- or D- amino acids consists of three steps:

- (i) chemical and/or enzymatic racemization of 5-substituted hydantoins
- (ii) ring opening hydrolysis achieved by a hydantoinase
25 and
- (iii) hydrolysis of the N-carbamoyl amino acid produced by hydantoinase to the amino acid by carbamoylase.

Arthrobacter aurescens DSM 3747 is one of the few isolated microorganisms capable of converting 5-monosubstituted
30 hydantoins to L-amino acids. The disadvantage of using A. aurescens cells as biocatalyst is the low enzyme activity. Especially the L-N-carbamoylase is the bottleneck for most

substrates leading to an increase of the intermediate L-N-carbamoyl amino acid in the cell, which is not further converted to the corresponding amino acid. By combining the purified enzymes bottlenecks could be avoided but due to
5 the low amounts of enzymes in the cells and loss of activity during the many necessary purification steps this process is not cost-effective.

All three genes encoding for the racemase *hyuA* (seq. 11), the L-specific hydantoinase *hyuH* (seq. 9) and the
10 stereoselective L-N-carbamoylase (seq. 7) have been cloned in *E. coli* separately and expressed to high levels (about 10 % of the total cell protein) (DE 19913741; J. Biotechnol., to be published). For in vitro catalysis the enzymes from the three recombinant strains can be produced
15 and purified more cost-effective than from the *Arthrobacter aurescens* strain. Regarding the different enzyme activities towards the various substrates the enzymes can be combined in enzyme reactors at ratios optimized for each reaction.

It is an object of this invention to provide a further
20 possibility of how a racemase, a hydantoinase and a D- or L-specific carbamoylase can act together in a process for the production of enantiomerically enriched amino acids from 5-monosubstituted hydantoins. Especially, this possibility should be suitable to be implemented in
25 processes on technical scale, that is to say it has to be most cost-effective.

This is done by using a whole cell catalyst according to claim 1. Further preferred catalysts are subjects to claims depending from claim 1. Claims 6 to 9 are directed to a
30 process for the production of the whole cell catalyst of the invention. Claims 10 and 11 protect a process for the production of enantiomerically enriched amino acids using the catalyst according to the invention.

Using whole cell catalysts comprising cloned genes encoding for a hydantoinase, for a hydantoin racemase and a D- or L-specific carbamoylase for the conversion of 5-monosubstituted hydantoins to L- or D-amino acids results in a fast and complete conversion of racemic mixtures of hydantoins to the corresponding L- or D-amino acids on industrial scale. This significantly reduces the production costs due to a reduction of fermentation and purification costs because all enzymes are produced in one strain.

Advantageously, a bacteria is used as cell, because of high reproduction rates and easy growing conditions to be applied. There are several bacteria known to the skilled worker which can be utilized in this respect. Preferably a *Escheria coli* can be used as cell and expression system in this regard (Yanisch-Perron et al. Gene (1985), 33, 103-109).

It is another positive embodiment of this invention that in principle all genes encoding for the hydantoinase, racemase and carbamoylase known to the artisan can be taken to be expressed in the whole cell catalyst. Preferably all genes can be taken from DSM 3747 (seq. 7, 9, 11).

The enzymes to be incorporated in the genetic code of the whole cell catalyst naturally possess different turnover rates. It is a drawback if the rates of co-working enzymes are not in line and intermediates accumulate during the production inside the cell. The overexpression of the hydantoinase gene in *E. coli* leads to the formation of inclusion bodies (Wiese et al., in preparation), which is unfavourable for a well balanced coexpression of all the three enzymes. Therefore, various attempts to "fine tune" the expression of these genes have been made. This can be done advantageously by overexpressing the hydantoinase genes in question according to their turnover rates. According to the DSM 3747-System the hydantoinase gene is overexpresses from plasmids with reduced copy numbers.

A further embodiment of the instant invention is directed to a process for the production of the whole cell catalyst according to the invention. In principle all plasmids known to the skilled worker can serve to carry the gene into the expression system. Preferably, plasmids derived from pSC101, pACYC184 or pBR322 are used to produce the catalyst. Most preferably plasmids pBW31 and pBW32, pBW34 and pBW35, pBW34 and pBW53, pBW32 or pBW34 are used in this respect. For the skilled worker plasmids and methods to produce plasmids can be deduced from Studier et al., Methods Enzymol. 1990, 185, 61-69 or brochures of Novagen, Promega, New England Biolabs, Clontech or Gibco BRL. More applicable plasmids, vectors can be found in: DNA cloning: a practical approach. Volume I-III, edited by D. M. Glover, IRL Press Ltd., Oxford, Washington DC, 1985, 1987; Denhardt, D. T. and Colasanti, J.: A survey of vectors for regulating expression of cloned DNA in E. coli. In: Rodriguez, R.L. and Denhardt, D. T (eds), Vectors, Butterworth, Stoneham, MA, 1987, pp179-204; Gene expression technology. In: Goeddel, D. V. (eds), Methods in Enzymology, Volume 185, Academic Press, Inc., San Diego, 1990; Sambrook, J., Fritsch, E.F. and Maniatis, T. 1989. Molecular cloning: a laboratory manual, 2nd ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. They are incorporated by reference herewith.

Over-expression can be accomplished by means known to the skilled artisan, e.g. using constitutive or inducible expression systems as reviewed by Makrides (Makrides, 1996, Microbiol. Rev. 60, no. 3, 512-538)

Preferably, for expression of the enzymes a rhamnose inducible E. coli promoter cassette is used.

In addition, primers useful for the amplification of the gene of the invention in a PCR are protected similarly. Primers which are feasible are for example, primers S988 (seq. 6), S2480 (seq. 1), S2248 (seq. 2), S2249 (seq. 3),

S2517 (seq. 4) or S2518 (seq. 5). Furthermore, all other primers which could serve to carry out this invention and which are known to the artisan are deemed to be useful in this sense. The finding of a suitable primer is done by
5 comparison of known DNA-sequences or translation of amino acid sequences into the codon of the organism in question (e.g. for Streptomyces: Wright et al., Gene 1992, 113, 55-65). Similarities in amino acid sequences of proteins of so called superfamilies are useful in this regard, too
10 (Firestine et al., Chemistry & Biology 1996, 3, 779-783). Additional information can be found in Oligonucleotide synthesis: a practical approach, edited by M.J. Gait, IRL Press Ltd, Oxford Washington DC, 1984; PCR Protocols: A guide to methods and applications, edited by M.A. Innis,
15 D.H. Gelfound, J.J. Sninsky and T.J. White. Academic Press, Inc., San Diego, 1990. Those strategies are incorporated by reference herewith.

Another aspect of the invention is a process for the production of enantiomerically enriched amino acids, which
20 utilizes a whole cell catalyst according to the invention. Furthermore, a process is preferred that is performed in an enzyme-membrane-reactor (DE 19910691.6).

To adopt the turnover rate of all enzymes expressed in the whole cell catalyst to each other there are different
25 methods to achieve this.

a) The genes are expressed with different promoters. The gene with the lowest activity is combined with the strongest promoter and vice versa. A disadvantage would be that for each gene a different inductor is necessary to
30 induce the expression of all genes.

b) The genes are expressed with one promoter on a polycistronic messenger. The ratios of synthesis of the enzymes is influenced by changing or by mutation of the translation initiation region of each gene (the ribosomal

binding site) which determines the efficiency of protein synthesis. This principle is realized in operons of microorganisms. The disadvantage is that the efficiency of a translation initiation region can not be predicted which means that for each gene many changes in the translation initiation region have to be made and tested (Grifantini et al., 1998, Microbiology, 144, 947-954).

c) The enzyme activity of each enzyme can be changed by mutation using error prone PCR (Fromant et al., 1995, Anal. Biochem. 224, 347-353) and DNA shuffling (Stemmer, 1994, Nature 370, 389-391). Again, this is very time consuming and costly.

d) Instead of mutagenizing genes to optimize their function in a reaction cascade, genes from different origins which encode enzymes with appropriate properties could be combined to an operon. This needs a large database describing such enzymes.

e) All genes are expressed from the same promoter but from replicons with different copy numbers. This can be the chromosome (single copy) or plasmids with low, moderate and high copy numbers. By constructing various compatible plasmids with different copy numbers and antibiotic markers carrying each the same cassette with the promoter and a polylinker sequence, genes of interest can be integrated into the plasmids in one step and the plasmids combined within one strain. This method allows a fast construction and testing of many combinations and with just one inducer in one fermentation all genes are expressed at different levels according to the plasmid copy number.

The following paragraphs show the transformation of Hydantoins to enantiomerically enriched amino acids.

Expression of the *hyuA* gene (seq. 11) is necessary for complete substrate conversion. Figure 1 shows the time

course of conversions with E.coli BW3110 containing pAW229 and pBW31. pAW 229 contains the carbamoylase gene on a pACYC plasmid, pBW31 is a pBR derivative and carries the hydantoinase gene. After consumption of 50% of the substrate, the reaction almost stops completely, since spontaneous racemisation of IMH is very slow (Syldatk et. al., "Biocatalytic production of amino acids and derivatives" (1992), Hanser publishers, New York, pp. 75-176). As can be seen from figure 2, bringing the racemase (seq. 11) into the system by using pBW31 and pBW32, the pACYC plasmid with the carbamoylase and the racemase gene, enables complete conversion of the substrate. After 4.5 hours induction at 30°C 200 µl permeabilized cells were prepared as described above and were incubated with 800 µl of 2 mM D,L-IMH.

The E. coli strain BW3110H with the chromosomally integrated hydantoinase gene was transformed with pBW32 (Figure 3), the pACYC plasmid containing the carbamoylase and the racemase gene, or with pBW34 (Figure 4), the pBR plasmid containing the carbamoylase and the racemase gene. Cells were induced at 25°C for 8.5 hours (pBW32), or for 11.5 hours (pBW34). Cell harvesting and permeabilization took place as described above.

Figure 5 shows E. coli BW3110 cells with pBW31 (the pBR plasmid which carries the hydantoinase gene) and pBW32 (the pACYC plasmid with the carbamoylase and racemase genes). Cells were induced 10 hours at 30°C.

The combination of pBW31 and 32 enables fast and complete conversion from D-L-IMH to tryptophane. The intermediate is formed up to a concentration of 0.4 mM.

E. coli BW3110 transformed with the plasmids pBW34 (the pBR plasmid with the carbamoylase and the racemase genes) and pBW35 (the pACYC plasmid with the hydantoinase gene) was taken for this conversion. Cells were induced for 10 hours at 30°C (Fig. 6). The combination of pBW34 and 35 shows an

accumulation of the intermediate up to over 1mM. The product formation takes place at a lower rate than seen in figure 5.

Plasmid pBW34 (the pBR plasmid with the carbamoylase and
5 the racemase genes) was combined with pBW53 (the pSC101 plasmid with the hydantoinase gene). Induction took place for 10 hours at 30°C (Fig 7). In this case a fast conversion of IMH to tryptophane takes place. Formation of the intermediate is strongly reduced and product formation
10 is faster than seen in figure 5, so that the combination of pBW34 and pBW53 is most favourable for the process.

The present invention shows a new and superior way to combine a hydantoinase, a hydantoin racemase and a carbamoylase in a whole cell catalysator. It is this
15 possibility that renders instant invention to a proper method for the production of enantiomerically enriched amino acids from hydantoins due to reduction of catalyst production costs.

Enantiomerically enriched means that one antipode of a
20 chiral compound is the major component in a mixture of both antipodes.

Amino acid denotes within the framework of this invention all compounds comprising a primary amine function connected to a carboxylic acid group via one intermediate C-atom (α -
25 C-atom). This α -C-atom bears only one further residue. Nevertheless all natural and unnatural amino acids are deemed to be encompassed. Preferred unnatural amino acids are those mentioned in DE 19903268.8.

Genes encoding for a peptide sequence are to be understood
30 as all genes possible with regard to the degeneration of the genetic code.

The microorganism DSM 3747 is disposed at Deutsche Sammlung für Mikroorganismen und Zellkulturen.

Examples:

Bacterial strains, plasmids and growth conditions:

E. coli JM109 (Yanisch-Perron et al. Gene (1985), 33, 103-109) was used for cloning procedures involving the hyuC (seq. 7), hyuH (seq. 9) and hyuA (seq. 11) genes from Arthrobacter aurescens DSM 3747 (Groß et al., Biotech. Tech. (1987), 2, 85-90). E. coli BW3110 (Wilms et al, in preparation), a derivative of E. coli W3110 (Hill and Harnish, 1981 Proc. Natl. Acad. Sci USA 78, 7069-7072) was used for coexpression for the genes mentioned above. E. coli strains were either grown in LB liquid medium or on LB-agar plates (Luria et al., 1960, Virology 12, 348-390), both supplemented with 100 µg/ml ampicillin and / or 25µg/ml chloramphenicol to select plasmid carrying strains. The cultures were grown at 37°C, for heterologous gene expression growth temperature was reduced to 30°C or 25°C.

General protocols:

All of the recombinant DNA techniques were standard methods (Sambrook et al., Molecular Cloning: A laboratory manual (1989), Cold Spring Harbour Laboratory Press, New York). PCR reactions were performed either with Pwo Polymerase or the Expand™ Long Template PCR System by following the recommendations of Roche Diagnostics.

Coexpression of hyuA, hyuC, and hyuH in E. coli:

For coexpression of the racemase gene hyuA, the carbamoylase gene hyuC, and the hydantoinase gene hyuH in E. coli, several constructions with different features were made. To obtain comparable expression levels of the genes, variations in the copy number of plasmids were used. High copy plasmids like pBR plasmids (Bolivar et al., 1977, Gene 22, 277-288) have a copy number of 40-50. PACYC184 plasmids (Chang and Cohen, 1978, J. Bacteriol., 1141-1156) have a copy number of 10-15. PSC101 plasmids (Cohen et al., 1973, Proc. Natl. Acad. Sci. USA, 70, 3240-3244) have a copy

number of 5-10. A copy number of 1 is achieved by inserting the gene into the E. coli chromosome.

The plasmid features are summarized in table1:

plasmid name	ori	copy number	resistance	hyu - genes
pAW229	pACYC	10-15	cam	hyuC
pBW31	pBR	40-50	amp	hyuH
pBW32	pACYC	10-15	cam	hyuC + hyuA
pBW34	pBR	40-50	amp	hyuC + hyuA
pBW35	pACYC	10-15	cam	hyuH
pBW53	pSC101	5-10	cam	hyuH

5

Abbreviations: hyu: hydantoin utilizing

hyuA: racemase gene (seq. 11)

hyuC: carbamoylase gene (seq. 7)

hyuH: hydantoinase gene (seq. 9)

10 amp: ampicillin resistance (β -lactamase gene)

cam: chloramphenicol resistance
(chloramphenicol acetyl transferase gene)

15

The hydantoinase gene *hyuH* was also expressed using the strain BW3110H, which carries a chromosomal insertion of the *hyuH* gene.

5 All constructs enable transcriptional regulation of gene expression by the *rhaBAD* promoter.

For coexpression of the carbamoylase gene *hyuC* and the hydantoinase gene *hyuH* pAW229 and pBW31 are transformed into *E. coli* BW3110.

10 For coexpression of the racemase gene *hyuA*, the carbamoylase gene *hyuC* and the hydantoinase gene *hyuH*, pBW31 and pBW32, pBW34 and pBW35, or pBW34 and pBW53 are suitable combinations in *E. coli* BW3110.

To achieve coexpression of all three Enzymes in *E. coli* BW3110H, pBW32 or pBW34 can be used.

15 Construction of the plasmids:

pAW229 was obtained by cleaving pAW178 (Wilms et al., J. Biotechnol. (1999), 68, 101-113) with the restriction enzymes NdeI and BamHI and ligating the 1241bp fragment containing the *hyuC* gene into pJOE2962 (Altenbuchner, 20 unpublished), which was cut with the same restriction enzymes.

pBW31 was constructed by cleaving pAW92 (Wiese et al., in preparation) with the restriction enzymes EcoRI and BamHI and ligating the 1436bp fragment containing the *hyuH* gene 25 into pBW22, which was cut with the same restriction enzymes.

pBW32 was obtained by PCR amplification of the *hyuA* gene using the primers S988 (5'-AGGCTGAAAATCTTCTCT-3') (seq. 6) and S2480 (5'-AAAAAAGCTTTTAAGAAGGAGATATACATA-3') (seq. 1) 30 and pAW210 (Wiese et al., in preparation) as template. Included in primer S2480 is a shine dalgarno sequence for translation initiation. The fragment was inserted into the HindIII site of pAW229.

pBW34 was created by inserting the *hyuA* PCR fragment 35 described above into the HindIII site of pBW24. pBW24 was

obtained by cleaving pAW178 (Wilms et al, J. Biotechnol. (1999), 68, 101-113) with NdeI and HindIII and ligating the 1261bp long fragment containing the hyuC gene into pBW22, which was cut with the same restriction enzymes. pBW22 was
5 constructed by PCR amplifying of the "cer"-region from the colE1 plasmid using the primers S2248 (5'-AAA GCA TGC ATG GCC CTT CGC TGG GAT-3') (seq. 2) and S2249 (5'-AAA GCA TGC ATG GCT ACG AGG GCA-3') (seq. 3). The 268bp fragment was cut with the restriction enzyme SphI and inserted in the
10 vector pJOE2775 (Krebsfänger et al., 1998, Enzyme Microb. Technol. 22, 219-224) which was cut with the same restriction enzyme.

pBW35 was constructed by cleaving pBW31 with the restriction enzymes NdeI and BamHI. The 1379bp fragment
15 containing hyuH was inserted into pAW229, which was cut with the same restriction enzymes.

pBW53 was obtained by cleaving pBW31 with the restriction enzymes SphI and BamHI. The 1534bp fragment containing the hyuH gene and the rhamnose promoter was inserted into pSB27
20 (Baumann, Dissertation, Universität Stuttgart, 1996), which was cut with the same restriction enzymes.

Construction of the chromosomal integrate of hyuH into the rhamnose operon:

A 3.5kb fragment from the E. coli rhamnose operon was
25 amplified using the primers S2517 (5'-AAACAAGATCTCGCGACTGG-3') (seq. 4) and S2518 (5'-AAAAAGATCTTTATCAGGCCTACAACTGTTG-3') (seq. 5) and E. coli chromosomal DNA as template. The fragment was cut with the restriction enzyme BglII and inserted into the vector pIC20H (Marsh et al., 1984, Gene
30 32, 481-485), which was cut with the restriction enzymes BamHI and BglII, to get pBW39. PBW31 was cut with the restriction enzymes EcoRI and BamHI. The 1436bp fragment containing the hyuH gene was inserted into the vector pBW39, which was also cut with the same restriction
35 enzymes, to get pBW40. A 2.9kb fragment was amplified using the primers S2517 and S2518 and pBW40 as a template. This

- fragment was cut with BglII and inserted into the vector pJOE2114 (Altenbuchner, unpublished) which was also cut with BglII to get pBW45. pBW45 was cut with BglII and SphI. The resulting 2.9kb rhaS-rhaP-hyuH-rhaA fragment was
- 5 inserted into the gene replacement vector pK03 (Link et al, 1997, J. Bacteriol., 179, 20, 6228-6237), which was cut with BamHI. The gene replacement was carried out according to the authors' instructions. Positive insertion events were screened using MacConckey Rhamnose plates.
- 10 Preparation of cells and activity measurements:
For induction of the *rhaBAD* promoter strains with two plasmids were grown in LB_{amp+cam}, strains with one plasmid in LB_{amp} or LB_{cam} respectively to OD₆₀₀ = 0.3-0.5. Then L-rhamnose was added to a final concentration of 0.1 g l⁻¹
- 15 and the cultivation was continued to a final OD of approximately 5. If not indicated separately, for small scale enzyme measurements cells corresponding to OD₆₀₀ of 20 were harvested, washed in 1 ml 0.2 M Tris pH 7.0 and resuspended in 1 ml 0.2 M Tris pH 7.0, 1 mM MnCl₂. 10 µl
- 20 toluene was added for permeabilizing the cell membranes. After 30min of incubation at 37°C 200 µl of this cell suspension were added to 800 µl of 2 mM D,L-Indolylmethylhydantoin (IMH) in 0.1 M Tris pH 8.5, mixed and shaken at 37°C. This cell amount corresponds to
- 25 approximately 5-6 mg cell wet weight. Samples were taken regularly. The reaction was stopped by adding 14% trichloroacetic acid. The time course of product and educt concentrations was determined using HPLC analysis. The HPLC-system was equipped with a RP-18 column as described
- 30 previously for the determination of hydantoin derivatives and N-carbamoyl amino acids (May et al., 1998, J. Biotechnol., 26, 61 (1): 1-13). UV-absorption was measured at 280 nm and the mobile phase (0.3% (v/v) phosphoric acid (80%) and methanol (20%; v/v)) was pumped with a flow rate
- 35 of 1.0 ml min⁻¹.

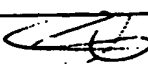
PCT

990160 AM

Original (for SUBMISSION) - printed on 24.08.2000 02:51:38 PM

0-1	Form - PCT/RO/134 (EASY) Indications Relating to Deposited Microorganism(s) or Other Biological Material (PCT Rule 13bis)	
0-1-1	Prepared using	PCT-EASY Version 2.91 (updated 01.07.2000)
0-2	International Application No.	
0-3	Applicant's or agent's file reference	990160 AM
1	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
1-1	page	8
1-2	line	32
1-3	Identification of Deposit	
1-3-1	Name of depositary institution	DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH
1-3-2	Address of depositary institution	Mascheroder Weg 1b, D-38124 Braunschweig, Germany
1-3-3	Date of deposit	
1-3-4	Accession Number	DSMZ 3747
1-4	Additional Indications	NONE
1-5	Designated States for Which Indications are Made	all designated States
1-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

FOR RECEIVING OFFICE USE ONLY

0-4	This form was received with the international application: (yes or no)	31.08.00
0-4-1	Authorized officer	 Mrs. T. Bröckner-Tetzlauer

FOR INTERNATIONAL BUREAU USE ONLY

0-5	This form was received by the international Bureau on:	
0-5-1	Authorized officer	

Claims:

1. Whole cell catalyst for the conversion of 5-monosubstituted hydantoins to L- or D-amino acids comprising cloned genes encoding for a hydantoinase,
5 for a hydantoin racemase and a D- or L-specific carbamoylase.
2. Catalyst according to claim 1, characterized in that a bacteria is used as cell.
- 10 3. Catalyst according to claim 1 and 2, characterized in that Escherichia coli is used as cell.
4. Catalyst according to one or more of preceding claims, characterized in that
15 the genes encoding for the hydantoinase, racemase and carbamoylase is taken from DSM 3747.
5. Catalyst according to one or more of preceding claims, characterized in that
20 the genes are overexpressed in the cell according to their turnover rates.
6. Process for the production of a whole cell catalyst, characterized in that plasmids derived from pSC101, pACYC184 or pBR322 are used.
- 25 7. Process according to claim 6, characterized in that plasmids pBW31 and pBW32, pBW34 and pBW35, pBW34 and pBW53, pBW32 or pBW34 are used.
- 30 8. Process according to claim 6, characterized in that an E. coli strain with a chromosomally insertion of the hydantoinase gene is used.

9. Process according to claim 6,
characterized in that
a rhamnose inducible E. coli promoter cassette is
used.
- 5 10. Process according to claim 6,
characterized in that
primers S2480, S2248, S2249, S2517 or S2518 are used.
11. Process for the production of enantiomerically
enriched amino acids,
10 characterized in that
a whole cell catalyst according to claim 1 is used.
12. Process according to claim 11,
characterized in that
the process is performed in an enzyme-membrane-
15 reactor.
13. Process for the production of whole cell catalysts
characterized in that
all genes are expressed from the same promotor but
from plasmids with replicons with different copy
20 numbers.
14. Plasmids pBW31, pBW32, pBW34, pBW35, pBW53, AW229.
15. Primers S2480, S2248, S2249, S2517, S2518.
16. Microorganisms comprising plasmids according to claim
14.

AMENDED CLAIMS

[received by the International Bureau on 6 February 2001 (06.02.01);
original claims 1-16 replaced by new claims 1-15 (2 pages)]

1. Whole cell catalyst for the conversion of 5-monosubstituted hydantoins to L- or D-amino acids comprising cloned genes encoding for a hydantoinase, for a hydantoin racemase and a D- or L-specific carbamoylase, wherein the genes are overexpressed in the cell according to their turnover rates.
2. Catalyst according to claim 1, characterized in that a bacteria is used as cell.
3. Catalyst according to claim 1 and 2, characterized in that *Escherichia coli* is used as cell.
4. Catalyst according to one or more of preceding claims, characterized in that the genes encoding for the hydantoinase, racemase and carbamoylase is taken from DSM 3747.
5. Process for the production of a whole cell catalyst according to claim 1, characterized in that plasmids derived from pSC101, pACYC184 or pBR322 are used.
6. Process according to claim 5, characterized in that plasmids pBW31 and pBW32, pBW34 and pBW35, pBW34 and pBW53, pBW32 or pBW34 are used.
7. Process according to claim 5, characterized in that an *E. coli* strain with a chromosomally insertion of the hydantoinase gene is used.
8. Process according to claim 5, characterized in that a rhamnose inducible *E. coli* promoter cassette is used.

9. Process according to claim 5,
characterized in that
primers S2480, S2248, S2249, S2517 or S2518 are used.
10. Process for the production of enantiomerically enriched
amino acids,
characterized in that
a whole cell catalyst according to claim 1 is used.
11. Process according to claim 10,
characterized in that
the process is performed in an enzyme-membrane-reactor.
12. Process for the production of whole cell catalysts
according to claim 1
characterized in that
all genes are expressed from the same promotor but from
plasmids with replicons with different copy numbers.
13. Plasmids pBW31, pBW32, pBW34, pBW35, pBW53, AW229.
14. Primers S2480, S2248, S2249, S2517, S2518.
15. Microorganisms comprising plasmids according to claim 13.

1/10

Fig 1:

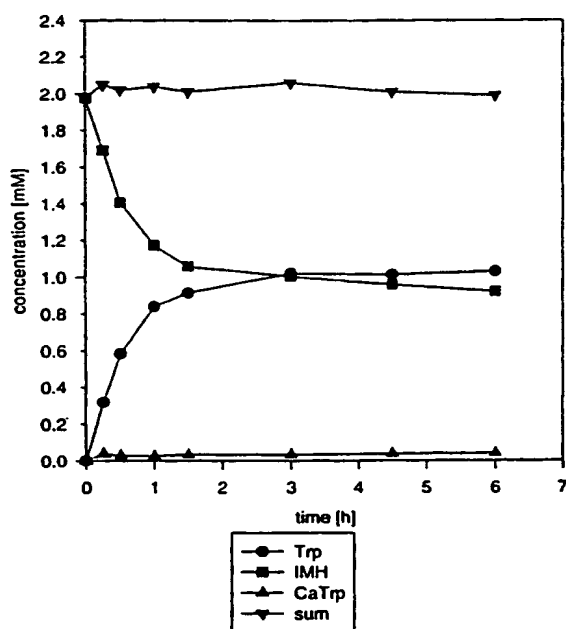
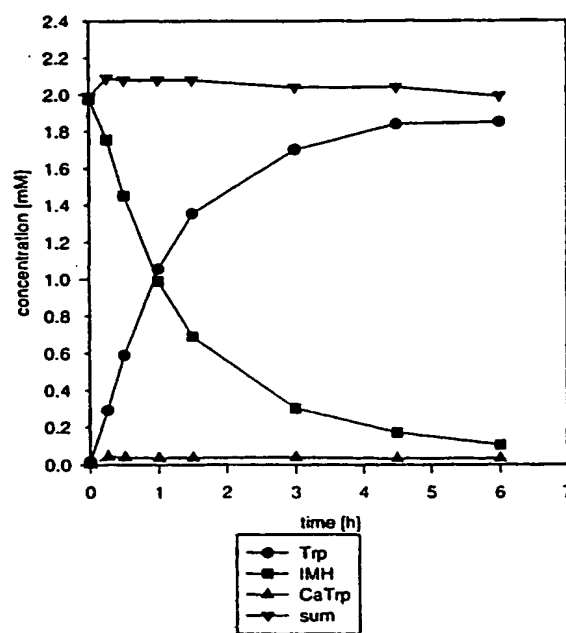


Fig. 2:



2/10

Fig. 3:

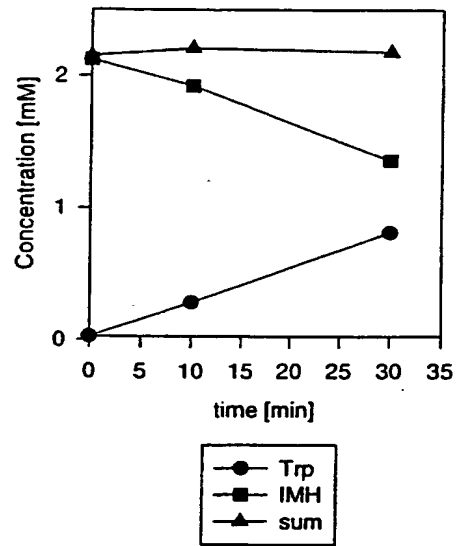
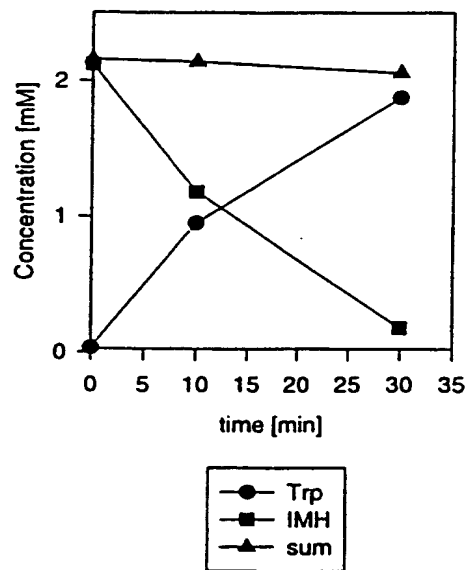


Fig. 4:



3110

Fig. 5:

5

10

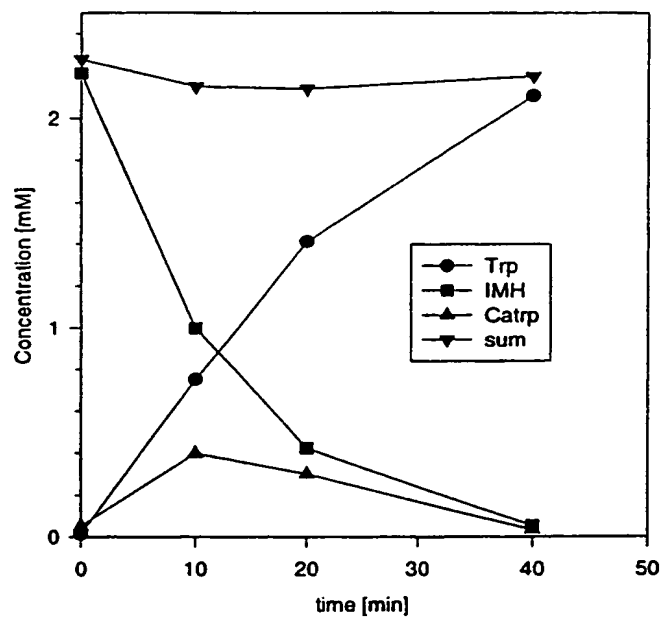
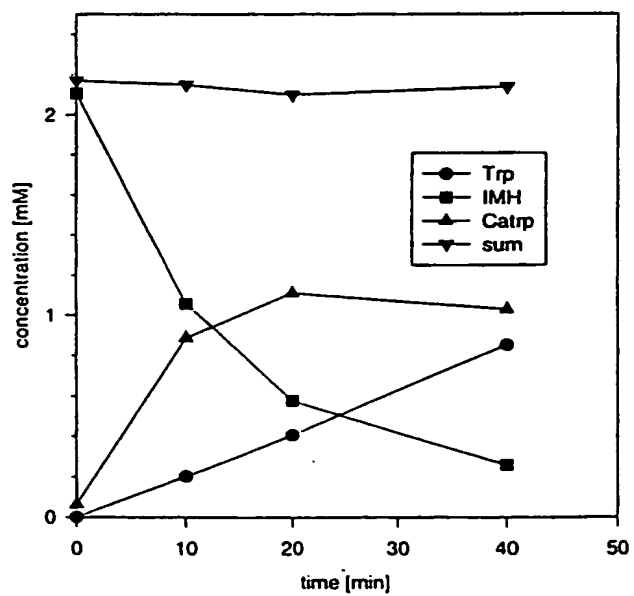


Fig.6:

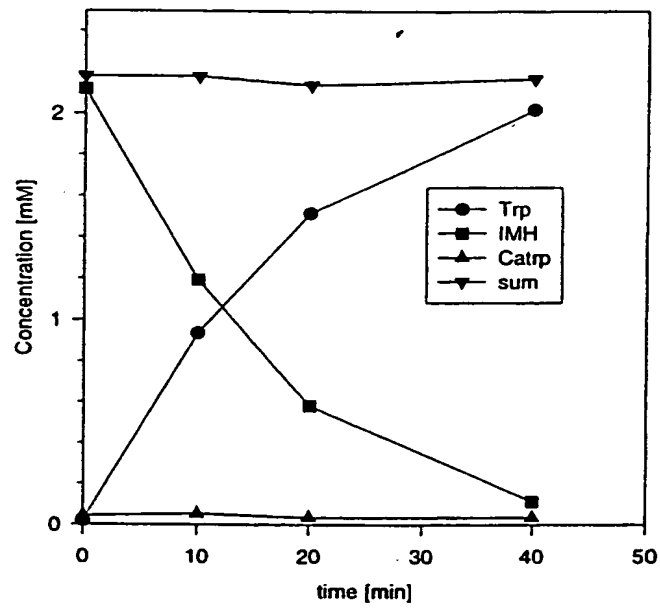
15

20



4110

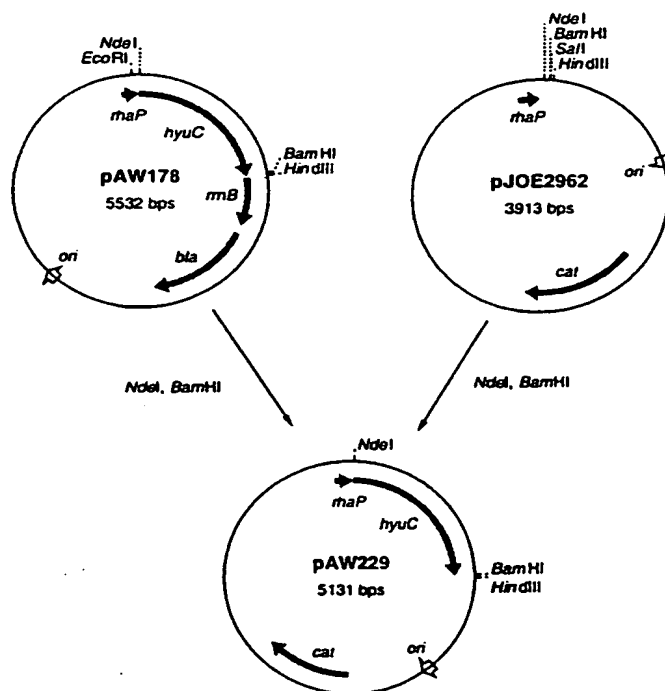
Fig. 7:



5/10

Fig. 8:

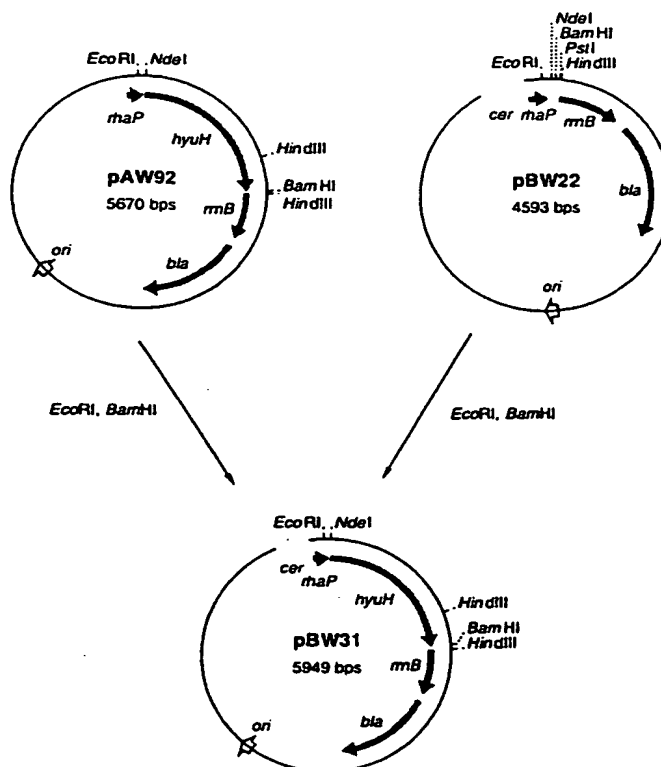
Construction of pAW229



6/10

Fig. 9:

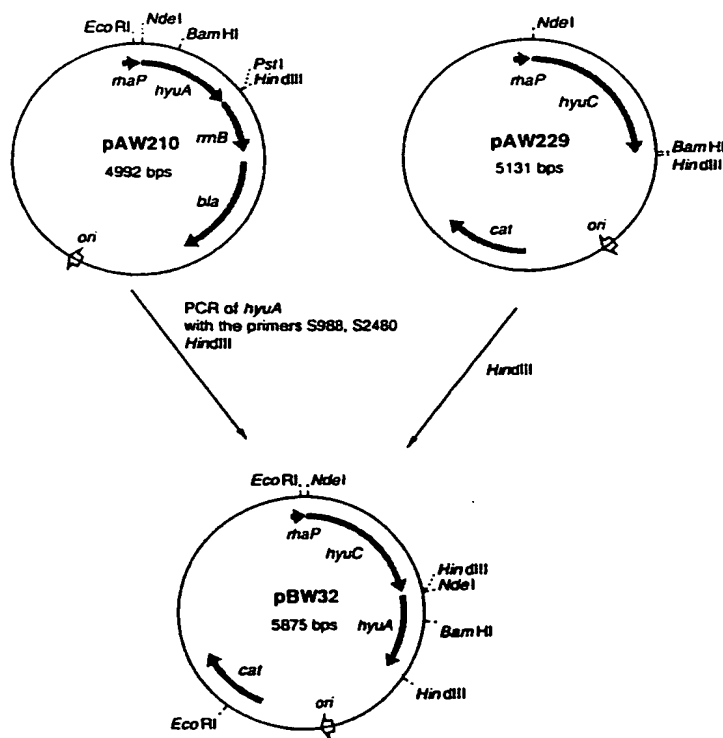
Construction of pBW31



7110

Fig. 10:

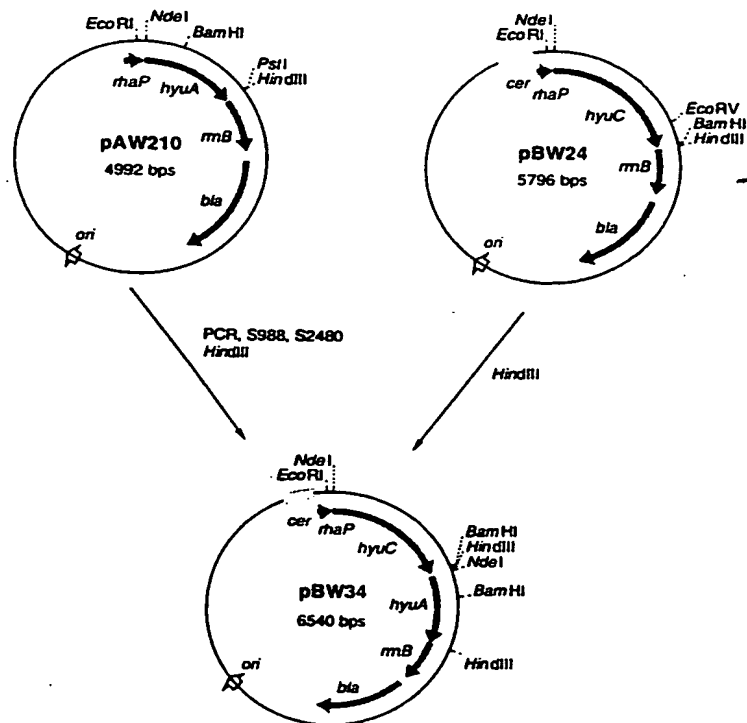
Construction of pBW32



8/10

Fig. 11:

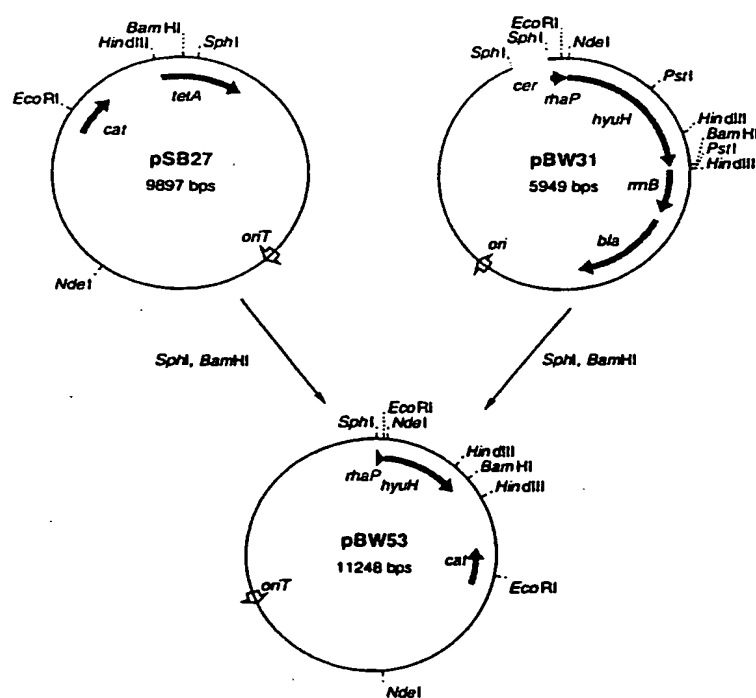
Construction of pBW34



9/10

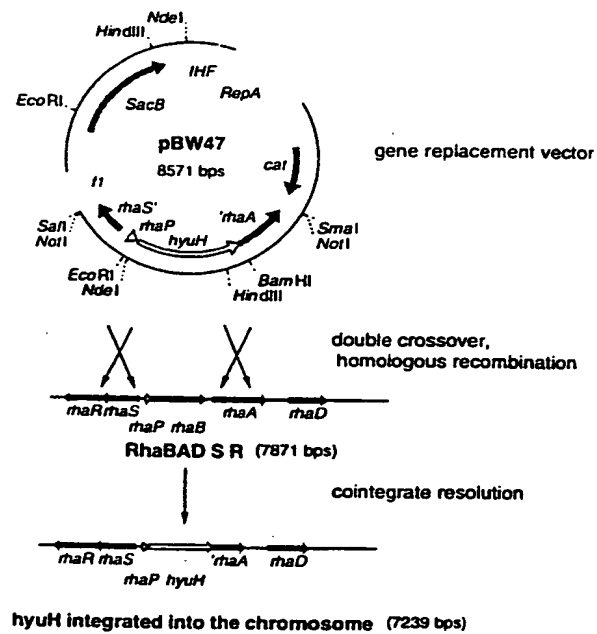
Fig. 12:

Construction of pBW53



10/10

Fig. 13:

Chromosomal insertion of *hyuH*

SEQUENCE LISTING

5 <110> Degussa-Huels Aktiengesellschaft
<120> Whole Cell Catalyst
<130> 990160 AM
10 <140>
<141>
<160> 11
15 <170> PatentIn Ver. 2.1
<210> 1
<211> 30
<212> DNA
20 <213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Primer
25 <400> 1
aaaaaagctt ttaagaagga gatatacata 30
<210> 2
30 <211> 27
<212> DNA
<213> Artificial Sequence
<220>
35 <223> Description of Artificial Sequence:Primer
<400> 2
aaagcatgca tggcccttcg ctgggat 27
40 <210> 3
<211> 24
<212> DNA
<213> Artificial Sequence
45 <220>
<223> Description of Artificial Sequence:Primer
<400> 3
50 aaagcatgca tggctacgag ggca 24
<210> 4
<211> 20
55 <212> DNA
<213> Artificial Sequence

2

<220>
 <223> Description of Artificial Sequence:Primer

<400> 4
 5 aaacaagatc tcgcgactgg 20

<210> 5
 <211> 31
 10 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer

15 <400> 5
 aaaaagatct ttatcaggcc tacaactgtt g 31

20 <210> 6
 <211> 1239
 <212> DNA
 <213> Arthrobacter aurescens

25 <220>
 <221> CDS
 <222> (1)..(1239)

30 <400> 6
 atg acc ctg cag aaa gcg caa gcg gcg cgc att gag aaa gag atc cgg 48
 Met Thr Leu Gln Lys Ala Gln Ala Ala Arg Ile Glu Lys Glu Ile Arg
 1 5 10 15

35 gag ctc tcc cgg ttc tcg gca gaa ggc ccc ggt gtt acc cgg ctg acc 96
 Glu Leu Ser Arg Phe Ser Ala Glu Gly Pro Gly Val Thr Arg Leu Thr
 20 25 30

40 tac act cca gag cat gcc gcc gcg cgg gaa acg ctc att gcg gct atg 144
 Tyr Thr Pro Glu His Ala Ala Ala Arg Glu Thr Leu Ile Ala Ala Met
 35 40 45

45 aaa gcg gcc gcc ttg agc gtt cgt gaa gac gca ctc gga aac atc atc 192
 Lys Ala Ala Ala Leu Ser Val Arg Glu Asp Ala Leu Gly Asn Ile Ile
 50 55 60

50 ggc cga cgt gaa ggc act gat ccg gag ctt cct gcg atc gcg gtc ggt 240
 Gly Arg Arg Glu Gly Thr Asp Pro Glu Leu Pro Ala Ile Ala Val Gly
 65 70 75 80

55 tca cac ttc gat tct gtc cga aac ggc ggg atg ttt gat ggc act gca 288
 Ser His Phe Asp Ser Val Arg Asn Gly Gly Met Phe Asp Gly Thr Ala
 85 90 95

60 ggc gtg gtg tgc gcc ctt gag gct gcc cgg gtg atg ctg gag aac ggc 336
 Gly Val Val Cys Ala Leu Glu Ala Ala Arg Val Met Leu Glu Asn Gly
 100 105 110

65 tac gtg aat cgg cat cca ttt gag ttc atc gcg atc gtg gag gag gaa 384
 Tyr Val Asn Arg His Pro Phe Glu Phe Ile Ala Ile Val Glu Glu Glu

	115	120	125	
5	ggg gcc cgc ttc agc agt ggc atg ttg ggc ggc cgg gcc att gca ggg Gly Ala Arg Phe Ser Ser Gly Met Leu Gly Gly Arg Ala Ile Ala Gly 130 135 140	432		
10	ttg gtc gcc gac agg gaa ctg gac tct ttg gtt gat gag gat gga gtg Leu Val Ala Asp Arg Glu Leu Asp Ser Leu Val Asp Glu Asp Gly Val 145 150 155 160	480		
15	tcc gtt agg cag gcg gct act gcc ttc ggc ttg aag ccg ggc gaa ctg Ser Val Arg Gln Ala Ala Thr Ala Phe Gly Leu Lys Pro Gly Glu Leu 165 170 175	528		
20	cag gct gca gcc cgc tcc gcg gcg gac ctg cgt gct ttt atc gaa cta Gln Ala Ala Ala Arg Ser Ala Ala Asp Leu Arg Ala Phe Ile Glu Leu 180 185 190	576		
25	cac att gaa caa gga ccg atc ctc gag cag gag caa ata gag atc gga His Ile Glu Gln Gly Pro Ile Leu Glu Gln Glu Ile Glu Ile Gly 195 200 205	624		
30	gtt gta acc tcc atc gtt ggc gtt cgc gca ttg cgg gtt gcc gtc aaa Val Val Thr Ser Ile Val Gly Val Arg Ala Leu Arg Val Ala Val Lys 210 215 220	672		
35	ggc aga agc gac cac gcc ggc aca acc ccc atg cac ctg cgc cag gat Gly Arg Ser Asp His Ala Gly Thr Thr Pro Met His Leu Arg Gln Asp 225 230 235 240	720		
40	gcg ctg gta ccc gcc gct ctc atg gtg agg gag gtc aac cgg ttc gtc Ala Leu Val Pro Ala Ala Leu Met Val Arg Glu Val Asn Arg Phe Val 245 250 255	768		
45	aac gag atc gcc gat ggc aca gtg gct acc gtt ggc cac ctc aca gtg Asn Glu Ile Ala Asp Gly Thr Val Ala Thr Val Gly His Leu Thr Val 260 265 270	816		
50	gcc ccc ggt gga ggc aac cag gtc ccg ggg gag gtg gac ttc aca ctg Ala Pro Gly Gly Gly Asn Gln Val Pro Gly Glu Val Asp Phe Thr Leu 275 280 285	864		
55	gac ctg cgt tct ccg cat gag gag tcg ctc cgc gtg ctg atc gac cgc Asp Leu Arg Ser Pro His Glu Glu Ser Leu Arg Val Leu Ile Asp Arg 290 295 300	912		
60	atc tcg gtc atg gtc ggc gag gtc gcc tcc cag gcc ggt gtg gct gcc Ile Ser Val Met Val Gly Glu Val Ala Ser Gln Ala Gly Val Ala Ala 305 310 315 320	960		
65	gat gtg gat gaa ttt ttc aat ctc agc ccg gtg cag ctg gct cct acc Asp Val Asp Glu Phe Asn Leu Ser Pro Val Gln Leu Ala Pro Thr 325 330 335	1008		
70	atg gtg gac gcc gtt cgc gaa gcg gcc tcg gcc ttg cag ttc aca cac Met Val Asp Ala Val Arg Glu Ala Ala Ser Ala Leu Gln Phe Thr His 340 345 350	1056		
75	cgg gat atc agc agt ggg gcg ggc cac gac tcg atg ttc atc gcc cag	1104		

4

Arg Asp Ile Ser Ser Gly Ala Gly His Asp Ser Met Phe Ile Ala Gln
 355 360 365
 5 gtc acg gac gtc gga atg gtt ttc gtt cca agc cgt gct ggc cgg agc 1152
 Val Thr Asp Val Gly Met Val Phe Val Pro Ser Arg Ala Gly Arg Ser
 370 375 380
 10 cac gtt ccc gaa gaa tgg acc gat ttc gat gac ctt cgc aaa gga act 1200
 His Val Pro Glu Glu Trp Thr Asp Phe Asp Asp Leu Arg Lys Gly Thr
 385 390 395 400
 gag gtt gtc ctc cgg gta atg aag gca ctt gac cgg taa 1239
 Glu Val Val Leu Arg Val Met Lys Ala Leu Asp Arg
 405 410
 15
 <210> 7
 <211> 413
 <212> PRT
 20 <213> *Arthrobacter aurescens*
 <400> 7
 Met Thr Leu Gln Lys Ala Gln Ala Ala Arg Ile Glu Lys Glu Ile Arg
 1 5 10 15
 25 Glu Leu Ser Arg Phe Ser Ala Glu Gly Pro Gly Val Thr Arg Leu Thr
 20 25 30
 30 Tyr Thr Pro Glu His Ala Ala Ala Arg Glu Thr Leu Ile Ala Ala Met
 35 40 45
 Lys Ala Ala Ala Leu Ser Val Arg Glu Asp Ala Leu Gly Asn Ile Ile
 50 55 60
 35 Gly Arg Arg Glu Gly Thr Asp Pro Glu Leu Pro Ala Ile Ala Val Gly
 65 70 75 80
 Ser His Phe Asp Ser Val Arg Asn Gly Gly Met Phe Asp Gly Thr Ala
 85 90 95
 40 Gly Val Val Cys Ala Leu Glu Ala Ala Arg Val Met Leu Glu Asn Gly
 100 105 110
 Tyr Val Asn Arg His Pro Phe Glu Phe Ile Ala Ile Val Glu Glu Glu
 115 120 125
 45 Gly Ala Arg Phe Ser Ser Gly Met Leu Gly Gly Arg Ala Ile Ala Gly
 130 135 140
 50 Leu Val Ala Asp Arg Glu Leu Asp Ser Leu Val Asp Glu Asp Gly Val
 145 150 155 160
 Ser Val Arg Gln Ala Ala Thr Ala Phe Gly Leu Lys Pro Gly Glu Leu
 165 170 175
 55 Gln Ala Ala Ala Arg Ser Ala Ala Asp Leu Arg Ala Phe Ile Glu Leu
 180 185 190
 His Ile Glu Gln Gly Pro Ile Leu Glu Gln Glu Gln Ile Glu Ile Gly

5

	195		200		205		
	Val Val Thr Ser Ile Val Gly Val Arg Ala Leu Arg Val Ala Val Lys						
	210		215		220		
5	Gly Arg Ser Asp His Ala Gly Thr Thr Pro Met His Leu Arg Gln Asp						
	225		230		235	240	
	Ala Leu Val Pro Ala Ala Leu Met Val Arg Glu Val Asn Arg Phe Val						
10		245		250		255	
	Asn Glu Ile Ala Asp Gly Thr Val Ala Thr Val Gly His Leu Thr Val						
		260		265		270	
15	Ala Pro Gly Gly Gly Asn Gln Val Pro Gly Glu Val Asp Phe Thr Leu						
		275		280		285	
	Asp Leu Arg Ser Pro His Glu Glu Ser Leu Arg Val Leu Ile Asp Arg						
20		290		295		300	
	Ile Ser Val Met Val Gly Glu Val Ala Ser Gln Ala Gly Val Ala Ala						
	305		310		315	320	
	Asp Val Asp Glu Phe Phe Asn Leu Ser Pro Val Gln Leu Ala Pro Thr						
25		325		330		335	
	Met Val Asp Ala Val Arg Glu Ala Ala Ser Ala Leu Gln Phe Thr His						
		340		345		350	
30	Arg Asp Ile Ser Ser Gly Ala Gly His Asp Ser Met Phe Ile Ala Gln						
		355		360		365	
	Val Thr Asp Val Gly Met Val Phe Val Pro Ser Arg Ala Gly Arg Ser						
		370		375		380	
35	His Val Pro Glu Glu Trp Thr Asp Phe Asp Asp Leu Arg Lys Gly Thr						
		385		390		395	400
	Glu Val Val Leu Arg Val Met Lys Ala Leu Asp Arg						
40		405		410			
	<210> 8						
	<211> 1377						
45	<212> DNA						
	<213> Arthrobacter aurescens						
	<220>						
	<221> CDS						
50	<222> (1)..(1377)						
	<400> 8						
	atg ttt gac gta ata gtt aag aac tgc cgt atg gtg tcc agc gac gga					48	
55	Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly						
	1	5		10		15	
	atc acc gag gca gac att ctg gtg aaa gac ggc aaa gtc gcc gca atc					96	
	Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile						
		20		25		30	

6

5	agc gcg gac aca cgt gat gtc gag gcc agc cga acc att gac gcg ggt Ser Ala Asp Thr Arg Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly	144
	35 40 45	
10	ggc aag ttc gtg atg ccg ggc gtg gtc gat gaa cat gtg cat atc atc Gly Lys Phe Val Met Pro Gly Val Val Asp Glu His Val His Ile Ile	192
	50 55 60	
15	gac atg gat ctc aag aac cgg tat ggc cgc ttc gaa ctc gat tcc gag Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu	240
	65 70 75 80	
20	tct gcg gcc gtg gga ggc atc acc acc atc atc gag atg ccg atc acc Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr	288
	85 90 95	
25	ttc cca ccc acc acc act ctg gac gcc ttc ctt gaa aag aag aag cag Phe Pro Pro Thr Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln	336
	100 105 110	
30	gcg ggg cag cgg ttg aaa gtt gac ttc gcg ctc tat gga ggt gga gtg Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val	384
	115 120 125	
35	ccg gga aac ctg ccc gag atc cgc aaa atg cac gac gcc ggc gct gtg Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val	432
	130 135 140	
40	ggc ttc aag tca atg atg gca gcc tca gtg ccg ggc atg ttc gac gcc Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala	480
	145 150 155 160	
45	gtc agc gac ggc gaa ctg ttc gaa atc ttc caa gag atc gca gcc tgt Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys	528
	165 170 175	
50	ggt tca gtc atc gtg gtt cat gcc gag aat gaa acg atc att caa gcg Gly Ser Val Ile Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala	576
	180 185 190	
55	ctc cag aag cag atc aag gcc gct ggc ggc aag gac atg gcc gcc tac Leu Gln Lys Gln Ile Lys Ala Ala Gly Gly Lys Asp Met Ala Ala Tyr	624
	195 200 205	
60	gag gca tcc caa cca gtt ttc cag gag aac gag gcc att cag cgt gcg Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala	672
	210 215 220	
65	ttg ctt ctg cag aaa gaa gcc ggc tgt cga ctg atc gtg ctt cac gtg Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val	720
	225 230 235 240	
70	agc aac cct gac ggc gtc gag tta ata cat cag gcg caa tcc gag ggt Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly	768
	245 250 255	
75	cag gac gtc cac tgc gag tcg ggt ccg cag tat ctg aat atc acc acg Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr	816

7

	260	265	270			
5	gac gac gcc gaa cga atc gga ccg tat atg aag gtc gcg ccg ccc gtc Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val	275	280	285	864	
10	cgc tca gcc gaa atg aac gtc agg tta tgg gaa caa ctc gag aac ggt Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly	290	295	300	912	
15	gtc atc gac acc ctt gga tca gat cat ggc gga cat cct gtc gag gac Val Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp	305	310	315	320	960
20	aaa gaa ccc ggc tgg aag gac gtg tgg aaa gcc ggc aac ggt gcg ctg Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu	325	330	335	1008	
25	ggc ctt gag aca tcc ctg cct atg atg ctg acc aac gga gtg aac aag Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys	340	345	350	1056	
30	ggc agg cta tcc ttg gaa cgc ctc gtc gag gtg atg tgc gag aaa cct Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro	355	360	365	1104	
35	gcg aag ctt ttt ggt atc tat ccg cag aag ggc acg cta cag gtt ggt Ala Lys Leu Phe Gly Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly	370	375	380	1152	
40	tcc gac gcc gat cta ctc atc ctc gat ctg gac att gac acc aaa gtg Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val	385	390	395	400	1200
45	gat gcg tcg cag ttc cga tcc ctg cat aag tac agc ccg ttc gac ggg Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly	405	410	415	1248	
50	atg ccc gtc acg ggt gca ccg gtt ctg acg atg gtg cgc gga acg gtg Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val	420	425	430	1296	
55	gtg gcc gag cag gga gaa gtt ctg gtc gag cag gga ttc ggc cag ttc Val Ala Glu Gln Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe	435	440	445	1344	
60	gtc acc cgt cac cac tac gag gcg tcg aag tga Val Thr Arg His His Tyr Glu Ala Ser Lys	450	455		1377	
65	<210> 9 <211> 459 <212> PRT <213> Arthrobacter aurescens					
70	<400> 9 Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly	1	5	10	15	

8

Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
 20 25 30

5 Ser Ala Asp Thr Arg Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
 35 40 45

Gly Lys Phe Val Met Pro Gly Val Val Asp Glu His Val His Ile Ile
 50 55 60

10 Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
 65 70 75 80

15 Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
 85 90 95

Phe Pro Pro Thr Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
 100 105 110

20 Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val
 115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
 130 135 140

25 Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
 145 150 155 160

30 Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
 165 170 175

Gly Ser Val Ile Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
 180 185 190

35 Leu Gln Lys Gln Ile Lys Ala Ala Gly Gly Lys Asp Met Ala Ala Tyr
 195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
 210 215 220

40 Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
 225 230 235 240

45 Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
 245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
 260 265 270

50 Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
 275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
 290 295 300

55 Val Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
 305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu

9

325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

5 Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

10 Ala Lys Leu Phe Gly Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

15 Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
420 425 430

20 Val Ala Glu Gln Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
435 440 445

25 Val Thr Arg His His Tyr Glu Ala Ser Lys
450 455

<210> 10
<211> 711
30 <212> DNA
<213> *Arthrobacter aurescens*

<220>
<221> CDS
35 <222> (1)..(711)

<400> 10
atg aga atc ctc gtg atc aac ccc aac agt tcc agc gcc ctt act gaa 48
Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
40 1 5 10 15

tcg gtt gcg gac gca gca caa caa gtt gtc gcg acc ggc acc ata att 96
Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
20 25 30

45 tct gcc atc aac ccc tcc aga gga ccc gcc gtc att gaa ggc agc ttt 144
Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
35 40 45

50 gac gaa gca ctg gcc acg ttc cat ctc att gaa gag gtg gag cgc gct 192
Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
50 55 60

55 gag cgg gaa aac ccg ccc gac gcc tac gtc atc gca tgt ttc ggg gat 240
Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Gly Asp
65 70 75 80

ccg gga ctt gac gcg gtc aag gag ctg act gac agg cca gtg gta gga 288
Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly

10

	85	90	95	
5	gtt gcc gaa gct gca atc cac atg tct tca ttc gtc gcg gcc acc ttc Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe 100 105 110			336
10	tcc att gtc agc atc ctc ccg agg gtc agg aaa cat ctg cac gaa ctg Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu 115 120 125			384
15	gta cgg caa gcg ggg gcg acg aat cgc ctc gcc tcc atc aag ctc cca Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro 130 135 140			432
20	aat ctg ggg gtg atg gcc ttc cat gag gac gaa cat gcc gca ctg gag Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu 145 150 155 160			480
25	acg ctc aaa caa gcc gcc aag gag gcg gtc cag gag gac ggc gcc gag Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu 165 170 175			528
30	tcg ata gtg ctc gga tgc gcc ggc atg gtg ggg ttt gcg cgt caa ctg Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu 180 185 190			576
35	agc gac gaa ctc ggc gtc cct gtc atc gac ccc gtc gag gca gct tgc Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys 195 200 205			624
40	cgc gtg gcc gag agt ttg gtc gct ctg ggc tac cag acc agc aaa gcg Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala 210 215 220			672
45	aac tcg tat caa aaa ccg aca gag aag cag tac ctc tag Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu 225 230 235			711
50	<210> 11 <211> 237 <212> PRT <213> Arthrobacter aurescens			
55	<400> 11 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu 1 5 10 15			
60	Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile 20 25 30			
65	Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe 35 40 45			
70	Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala 50 55 60			
75	Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Gly Asp 65 70 75 80			

14

Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
 85 90 95
 5 Val Ala Glu Ala Ala Ile His Met Ser Ser, Phe Val Ala Ala Thr Phe
 100 105 110
 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
 115 120 125
 10 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
 130 135 140
 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
 15 145 150 155 160
 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
 165 170 175
 20 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
 180 185 190
 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
 195 200 205
 25 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
 210 215 220
 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
 30 225 230 235
 335
 35 atg gtg gac gcc gtt cgc gaa gcg gcc tcg gcc ttg cag ttc aca cac 1056
 Met Val Asp Ala Val Arg Glu Ala Ala Ser Ala Leu Gln Phe Thr His
 340 345 350
 40 cgg gat atc agc agt ggg gcg ggc cac gac tcg atg ttc atc gcc cag 1104
 Arg Asp Ile Ser Ser Gly Ala Gly His Asp Ser Met Phe Ile Ala Gln
 355 360 365
 gtc acg gac gtc gga atg gtt ttc gtt cca agc cgt gct ggc cgg agc 1152
 45 Val Thr Asp Val Gly Met Val Phe Val Pro Ser Arg Ala Gly Arg Ser
 370 375 380
 cac gtt ccc gaa gaa tgg acc gat ttc gat gac ctt cgc aaa gga act 1200
 50 His Val Pro Glu Glu Trp Thr Asp Phe Asp Leu Arg Lys Gly Thr
 385 390 395 400
 gag gtt gtc ctc cgg gta atg aag gca ctt gac cgg taa 1239
 Glu Val Val Leu Arg Val Met Lys Ala Leu Asp Arg
 405 410
 55
 <210> 7
 <211> 413
 <212> PRT

12

<213> Arthrobacter aurescens

<400> 7

5 Met Thr Leu Gln Lys Ala Gln Ala Ala Arg Ile Glu Lys Glu Ile Arg
 1 5 10 15
 Glu Leu Ser Arg Phe Ser Ala Glu Gly Pro Gly Val Thr Arg Leu Thr
 20 25 30
 10 Tyr Thr Pro Glu His Ala Ala Ala Arg Glu Thr Leu Ile Ala Ala Met
 35 40 45
 Lys Ala Ala Ala Leu Ser Val Arg Glu Asp Ala Leu Gly Asn Ile Ile
 50 55 60
 15 Gly Arg Arg Glu Gly Thr Asp Pro Glu Leu Pro Ala Ile Ala Val Gly
 65 70 75 80
 20 Ser His Phe Asp Ser Val Arg Asn Gly Gly Met Phe Asp Gly Thr Ala
 85 90 95
 Gly Val Val Cys Ala Leu Glu Ala Ala Arg Val Met Leu Glu Asn Gly
 100 105 110
 25 Tyr Val Asn Arg His Pro Phe Glu Phe Ile Ala Ile Val Glu Glu Glu
 115 120 125
 Gly Ala Arg Phe Ser Ser Gly Met Leu Gly Gly Arg Ala Ile Ala Gly
 130 135 140
 30 Leu Val Ala Asp Arg Glu Leu Asp Ser Leu Val Asp Glu Asp Gly Val
 145 150 155 160
 35 Ser Val Arg Gln Ala Ala Thr Ala Phe Gly Leu Lys Pro Gly Glu Leu
 165 170 175
 Gln Ala Ala Ala Arg Ser Ala Ala Asp Leu Arg Ala Phe Ile Glu Leu
 180 185 190
 40 His Ile Glu Gln Gly Pro Ile Leu Glu Gln Glu Gln Ile Glu Ile Gly
 195 200 205
 Val Val Thr Ser Ile Val Gly Val Arg Ala Leu Arg Val Ala Val Lys
 210 215 220
 45 Gly Arg Ser Asp His Ala Gly Thr Thr Pro Met His Leu Arg Gln Asp
 225 230 235 240
 50 Ala Leu Val Pro Ala Ala Leu Met Val Arg Glu Val Asn Arg Phe Val
 245 250 255
 Asn Glu Ile Ala Asp Gly Thr Val Ala Thr Val Gly His Leu Thr Val
 260 265 270
 55 Ala Pro Gly Gly Gly Asn Gln Val Pro Gly Glu Val Asp Phe Thr Leu
 275 280 285
 Asp Leu Arg Ser Pro His Glu Glu Ser Leu Arg Val Leu Ile Asp Arg
 290 295 300

Ile Ser Val Met Val Gly Glu Val Ala Ser Gln Ala Gly Val Ala Ala
 305 310 315 320
 5 Asp Val Asp Glu Phe Phe Asn Leu Ser Pro, Val Gln Leu Ala Pro Thr
 325 330 335
 Met Val Asp Ala Val Arg Glu Ala Ala Ser Ala Leu Gln Phe Thr His
 340 345 350
 10 Arg Asp Ile Ser Ser Gly Ala Gly His Asp Ser Met Phe Ile Ala Gln
 355 360 365
 Val Thr Asp Val Gly Met Val Phe Val Pro Ser Arg Ala Gly Arg Ser
 15 370 375 380
 His Val Pro Glu Glu Trp Thr Asp Phe Asp Asp Leu Arg Lys Gly Thr
 385 390 395 400
 20 Glu Val Val Leu Arg Val Met Lys Ala Leu Asp Arg
 405 410
 <210> 8
 25 <211> 1377
 <212> DNA
 <213> *Arthrobacter aurescens*
 <220>
 30 <221> CDS
 <222> (1)..(1377)
 <400> 8
 35 atg ttt gac gta ata gtt aag aac tgc cgt atg gtg tcc agc gac gga 48
 Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
 1 5 10 15
 atc acc gag gca gac att ctg gtg aaa gac ggc aaa gtc gcc gca atc 96
 40 Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
 20 25 30
 agc gcg gac aca cgt gat gtc gag gcc agc cga acc att gac gcg ggt 144
 Ser Ala Asp Thr Arg Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
 35 40 45
 45 ggc aag ttc gtg atg ccg ggc gtg gtc gat gaa cat gtg cat atc atc 192
 Gly Lys Phe Val Met Pro Gly Val Val Asp Glu His Val His Ile Ile
 50 55 60
 50 gac atg gat ctc aag aac cgg tat ggc cgc ttc gaa ctc gat tcc gag 240
 Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
 65 70 75 80
 tct gcg gcc gtg gga ggc atc acc acc atc atc gag atg ccg atc acc 288
 55 Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
 85 90 95
 ttc cca ccc acc acc act ctg gac gcc ttc ctt gaa aag aag aag cag 336
 Phe Pro Pro Thr Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln

14

	100	105	110	
5	gcg ggg cag cgg ttg aaa gtt gac ttc gcg ctc tat gga ggt gga gtg Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val 115 120 125	384		
10	ccg gga aac ctg ccc gag atc cgc aaa atg cac gac gcc ggc gct gtg Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val 130 135 140	432		
15	ggc ttc aag tca atg atg gca gcc tca gtg ccg ggc atg ttc gac gcc Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala 145 150 155 160	480		
20	gtc agc gac ggc gaa ctg ttc gaa atc ttc caa gag atc gca gcc tgt Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys 165 170 175	528		
25	ggc tca gtc atc gtg gtt cat gcc gag aat gaa acg atc att caa ggc Gly Ser Val Ile Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala 180 185 190	576		
30	ctc cag aag cag atc aag gcc gct ggc ggc aag gac atg gcc gcc tac Leu Gln Lys Gln Ile Lys Ala Ala Gly Gly Lys Asp Met Ala Ala Tyr 195 200 205	624		
35	gag gca tcc caa cca gtt ttc cag gag aac gag gcc att cag cgt ggc Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala 210 215 220	672		
40	ttg ctt ctg cag aaa gaa gcc ggc tgt cga ctg atc gtg ctt cac gtg Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val 225 230 235 240	720		
45	agc aac cct gac ggc gtc gag tta ata cat cag gcg caa tcc gag ggt Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly 245 250 255	768		
50	cag gac gtc cac tgc gag tcg ggt ccg cag tat ctg aat atc acc acg Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr 260 265 270	816		
55	gac gac gcc gaa cga atc gga ccg tat atg aag gtc gcg ccg ccc gtc Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val 275 280 285	864		
60	cgc tca gcc gaa atg aac gtc agg tta tgg gaa caa ctc gag aac ggt Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly 290 295 300	912		
65	gtc atc gac acc ctt gga tca gat cat ggc gga cat cct gtc gag gac Val Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp 305 310 315 320	960		
70	aaa gaa ccc ggc tgg aag gac gtg tgg aaa gcc ggc aac ggt gcg ctg Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu 325 330 335	1008		
75	ggc ctt gag aca tcc ctg cct atg atg ctg acc aac gga gtg aac aag	1056		

15

	Gly	Leu	Glu	Thr	Ser	Leu	Pro	Met	Met	Leu	Thr	Asn	Gly	Val	Asn	Lys	
				340					345					350			
5	ggc	agg	cta	tcc	ttg	gaa	cgc	ctc	gtc	gag	gtg	atg	tgc	gag	aaa	cct	1104
	Gly	Arg	Leu	Ser	Leu	Glu	Arg	Leu	Val	Glu	Val	Met	Cys	Glu	Lys	Pro	
			355					360					365				
10	gcg	aag	ctt	ttt	ggt	atc	tat	ccg	cag	aag	ggc	acg	cta	cag	gtt	ggt	1152
	Ala	Lys	Leu	Phe	Gly	Ile	Tyr	Pro	Gln	Lys	Gly	Thr	Leu	Gln	Val	Gly	
			370				375					380					
15	tcc	gac	gcc	gat	cta	ctc	atc	ctc	gat	ctg	gac	att	gac	acc	aaa	gtg	1200
	Ser	Asp	Ala	Asp	Leu	Leu	Ile	Leu	Asp	Leu	Asp	Ile	Asp	Thr	Lys	Val	
			385				390				395					400	
20	gat	gcg	tcg	cag	ttc	cga	tcc	ctg	cat	aag	tac	agc	ccg	ttc	gac	ggg	1248
	Asp	Ala	Ser	Gln	Phe	Arg	Ser	Leu	His	Lys	Tyr	Ser	Pro	Phe	Asp	Gly	
					405					410					415		
25	atg	ccc	gtc	acg	ggt	gca	ccg	gtt	ctg	acg	atg	gtg	cgc	gga	acg	gtg	1296
	Met	Pro	Val	Thr	Gly	Ala	Pro	Val	Leu	Thr	Met	Val	Arg	Gly	Thr	Val	
					420				425					430			
30	gtg	gcc	gag	cag	gga	gaa	gtt	ctg	gtc	gag	cag	gga	ttc	ggc	cag	ttc	1344
	Val	Ala	Glu	Gln	Gly	Glu	Val	Leu	Val	Glu	Gln	Gly	Phe	Gly	Gln	Phe	
					435			440					445				
35	gtc	acc	cgt	cac	cac	tac	gag	gcg	tcg	aag	tga						1377
	Val	Thr	Arg	His	His	Tyr	Glu	Ala	Ser	Lys							
			450				455										
40	<210>	9															
	<211>	459															
	<212>	PRT															
	<213>	Arthrobacter	aure	scens													
45	<400>	9															
	Met	Phe	Asp	Val	Ile	Val	Lys	Asn	Cys	Arg	Met	Val	Ser	Ser	Asp	Gly	
		1				5				10					15		
50	Ile	Thr	Glu	Ala	Asp	Ile	Leu	Val	Lys	Asp	Gly	Lys	Val	Ala	Ala	Ile	
					20				25					30			
55	Ser	Ala	Asp	Thr	Arg	Asp	Val	Glu	Ala	Ser	Arg	Thr	Ile	Asp	Ala	Gly	
			35					40					45				
60	Gly	Lys	Phe	Val	Met	Pro	Gly	Val	Val	Asp	Glu	His	Val	His	Ile	Ile	
		50					55					60					
65	Asp	Met	Asp	Leu	Lys	Asn	Arg	Tyr	Gly	Arg	Phe	Glu	Leu	Asp	Ser	Glu	
		65				70				75						80	
70	Ser	Ala	Ala	Val	Gly	Gly	Ile	Thr	Thr	Ile	Ile	Glu	Met	Pro	Ile	Thr	
					85				90					95			
75	Phe	Pro	Pro	Thr	Thr	Thr	Leu	Asp	Ala	Phe	Leu	Glu	Lys	Lys	Lys	Gln	
				100					105					110			

16

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val
115 120 125

5 Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

10 Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Ile Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

15 Leu Gln Lys Gln Ile Lys Ala Ala Gly Gly Lys Asp Met Ala Ala Tyr
195 200 205

20 Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

25 Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

30 Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

35 Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Val Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

40 Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

45 Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

50 Ala Lys Leu Phe Gly Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

55 Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pr

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 00/08473

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/55 C12N15/61 C12P13/00 C12P13/22 C12P41/00
C12N1/21 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C12P C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
BIOSIS, MEDLINE, EPO-Internal, WPI Data, PAJ, STRAND, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WATABE K ET AL: "IDENTIFICATION AND SEQUENCING OF A GENE ENCODING A HYDANTOIN RACEMASE FROM THE NATIVE PLASMID OF PSEUDOMONAS-SP STRAIN NS671" JOURNAL OF BACTERIOLOGY, vol. 174, no. 11, 1992, pages 3461-3466, XP000944037 ISSN: 0021-9193 page 3461, left-hand column, paragraph 2 -page 3463, right-hand column, paragraph 2; figures 3,4 page 3465, right-hand column page 3466, left-hand column, paragraphs 3-5	1-3,5,6, 11
Y	page 3465, right-hand column, paragraph 1 -page 3466, left-hand column, paragraph 1	1-3,5,6, 11,13
Y	page 3462, left-hand column, paragraph 5 -page 3462, right-hand column, paragraph 1	9
Y	page 3462 -/--	4

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *G* document member of the same patent family

Date of the actual completion of the international search

11 December 2000

Date of mailing of the international search report

16.01.01

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl.
Fax: (+31-70) 340-3016

Authorized officer

Steffen, P

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 00/08473

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p style="text-align: center;">---</p> <p>GRIFANTINI RENATA ET AL: "Efficient conversion of 5-substituted hydantoins to D-alpha-amino acids using recombinant Escherichia coli strains." MICROBIOLOGY (READING), vol. 144, no. 4, April 1998 (1998-04), pages 947-954, XP002154848 ISSN: 1350-0872 page 949; figure 1 page 950, right-hand column, paragraph 2 -page 952, right-hand column, paragraph 1; table 4 page 953, left-hand column</p>	1-3,5,6, 11,13
X	<p style="text-align: center;">---</p> <p>SIEMANN MARTIN ET AL: "Characterization of serological properties of polyclonal antibodies produced against enzymes involved in the L-selective cleavage of hydantoin derivatives." BIOTECHNOLOGY LETTERS, vol. 15, no. 1, 1993, pages 1-6, XP000944249 ISSN: 0141-5492 page 1, paragraph 1 -page 2, paragraph 4 page 5; table 1 page 2; table 1</p>	14,16
Y		4
X	<p style="text-align: center;">---</p> <p>WILMS BURKHARD ET AL: "Cloning, nucleotide sequence and expression of a new L-N-carbamoylase gene from Arthrobacter aurescens DSM 3747 in E. coli." JOURNAL OF BIOTECHNOLOGY, vol. 68, no. 2-3, 19 February 1999 (1999-02-19), pages 101-113, XP004164275 ISSN: 0168-1656 page 102, right-hand column, paragraph 4 -page 103, left-hand column, paragraph 1 page 109, left-hand column page 103 -page 104, left-hand column</p>	14,16
Y		9
X	<p style="text-align: center;">---</p> <p>BLATTNER FREDERICK R ET AL: "The complete genome sequence of Escherichia coli K-12." SCIENCE (WASHINGTON D C), vol. 277, no. 5331, 1997, pages 1453-1462, XP002069950 ISSN: 0036-8075 page 1454, right-hand column, paragraph 3</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/-</p>	15

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 00/08473

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE GENBANK 'Online! NCBI; Acc No: J01566, 8 February 1996 (1996-02-08) LEBOWITZ, J.: "Plasmid ColE1, complete genome" retrieved from NCBI, accession no. http://www.ncbi.nlm.nih.gov:80/ Database accession no. <a href="http://www.ncbi.nlm.nih.gov:80/Genbank/ind
 ex.html">http://www.ncbi.nlm.nih.gov:80/Genbank/ind ex.html XP002154850 the whole document</p>	15
P, X	<p>MAY OLIVER ET AL: "Inverting enantioselectivity by directed evolution of hydantoinase for improved production of L-methionine." NATURE BIOTECHNOLOGY, vol. 18, no. 3, March 2000 (2000-03), pages 317-320, XP002154849 ISSN: 1087-0156 page 318, right-hand column, paragraph 2 -page 319, left-hand column, paragraph 1 page 319, right-hand column, paragraph 3 -page 320, left-hand column, paragraph 1</p>	1-16
P, X	<p>WIESE ANJA ET AL: "Hydantoin racemase from <i>Arthrobacter aurescens</i> DSM 3747: Heterologous expression, purification and characterization." JOURNAL OF BIOTECHNOLOGY, vol. 80, no. 3, 2000, pages 217-230, XP000943983 ISSN: 0168-1656 page 220, right-hand column, paragraph 2 -page 222, left-hand column, paragraph 1; figures 2,4</p>	1-16
A	<p>WATABE K ET AL: "CLONING AND SEQUENCE OF THE GENES INVOLVED IN THE CONVERSION OF 5-SUBSTITUTED HYDANTOINS TO THE CORRESPONDING L AMINO ACIDS FROM THE NATIVE PLASMID OF <i>PSEUDOMONAS</i>-SP STRAIN NS671" JOURNAL OF BACTERIOLOGY, vol. 174, no. 3, 1992, pages 962-969, XP000944036 ISSN: 0021-9193 the whole document</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 00/08473

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 6,8,9,13 (partially)
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 6,8,9,13 (partially)

Present claims 6, 8, 9 and 13 relate to an extremely large number of possible methods. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found, however, for only a very small proportion of the methods claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Consequently, the search has been carried out for those parts of the claims which appear to be supported and disclosed, namely when the whole cell catalyst as referred to in claims 6, 8, 9 and 13 is restricted to a whole cell catalyst according to claim 1.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.